AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of the Claims

1. (Currently Amended) A method for detecting a ~~genetic marker~~ polymorphism related to a genetic disease in a patient sample nucleic acid, comprising the steps of:

providing the patient sample nucleic acid containing ~~multiple loci~~ a first and a second loci having a first and second polymorphism, respectively, related to the genetic disease at a microarray site;

providing ~~at least one~~ a blocker that is complementary to ~~at least one~~ the first loci containing the first polymorphism related to the genetic disease ~~of the multiple loci contained in the patient sample nucleic acid~~;

hybridizing the ~~at least one~~ blocker with the first loci, ~~patient sample nucleic acid,~~ wherein ~~at least one loci containing the~~ ~~genetic marker~~ the second loci is unblocked;

providing a detectable discriminator that is capable of ~~binding~~ hybridizing with the ~~at least one unblocked~~ second loci containing the second polymorphism related to the genetic disease; [[and]]

hybridizing the detectable discriminator with the ~~at least one unblocked loci of the patient sample;~~ second loci containing the second polymorphism related to the genetic disease; and

detecting the ~~genetic marker~~ second polymorphism related to the genetic disease by detecting the presence of the discriminator at the microarray site.

2-4. (Canceled)

5. (Previously Presented) The method of claim 1, wherein different blockers are provided to different sites.

6. (Currently Amended) The method of claim 1, wherein the microarray site comprises a site of an actively addressable electronic microarray.

7. (Previously Presented) The method of claim 6, wherein the addressable electronic microarray includes a permeation layer.

8. (Previously Presented) The method of claim 1, wherein the patient sample is amplified.

9. (Currently Amended) The method of claim 8, wherein the amplification includes polymerase chain reaction (PCR).

10. (Withdrawn-Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 8, wherein the amplification includes ligase chain reaction (LCR).

11. (Withdrawn-Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 8, wherein the amplification ~~include~~ includes strand displacement amplification (SDA).

12. (Withdrawn-Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 8, wherein the amplification includes the transcription-based amplification system (TAS).

13. (Withdrawn-Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 8, wherein the amplification includes the self-sustained sequence replication system (3SR).

14. (Withdrawn-Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 8, wherein the amplification includes the Qβ replicase amplification system (Qβ).

15-16. (Canceled)

17. (Previously Presented) The method of claim 1, wherein at least two loci are unblocked.

18. (Previously Presented) The method of claim 1, further includes the step of performing a screening step.

19. (Previously Presented) The method of claim 1, wherein the patient sample nucleic acid comprises multiple segments containing different loci.

20. (Currently Amended) The method of claim 19, wherein the multiple segments containing different loci are affixed to the same microarray site.

21. (Withdrawn-Currently Amended) The method ~~for detecting members of a set of polymorphisms that occur at identified loci in samples of patient nucleic acid~~ of claim 19, wherein the multiple segments containing different loci are affixed to the different sites.

22. (Previously Presented) The method of claim 6, wherein the multiple patient samples are provided on multiple sites of the microarray.

23. (Currently Amended) The method of claim 1, further comprising the steps of:

providing a labeled amplification control that is capable of binding with the patient nucleic acid sample; and

hybridizing the labeled amplification control to the patient nucleic acid sample.

24. (Canceled)

25. (Currently Amended) The method of ~~claim 24~~ claim 1, wherein the genetic disease is cystic fibrosis.

26. (Canceled)

27. (Currently Amended) The method of claim 1, further comprising the steps of:

providing a stabilizer that is capable of binding with the patient nucleic acid sample adjacent the at least one discriminator; and

hybridizing the stabilizer to the patient nucleic acid sample.

28-44. (Canceled)